FIGURE 1

TGMV Rep, amino acids 110-179:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:2)

Ala 1 mutant:

TLVWGEFQVD G<u>AA</u>A<u>A</u>GGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:3)

Ala5 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>AAALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:15)

Ala4+5 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAALA</u> ASS<u>AAAALOI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:4)

Ala6 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IAAA</u>IPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:5)

Ala7 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIP<u>AAA</u>L FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:6)

Ala8 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL F<u>AFAA</u>LNSNL DRIFDKTPEP (SEQ ID NO:7)

Ala9 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNS<u>A</u>L <u>AA</u>IFDKTPEP (SEQ ID NO:8)

Ala13 mutant:

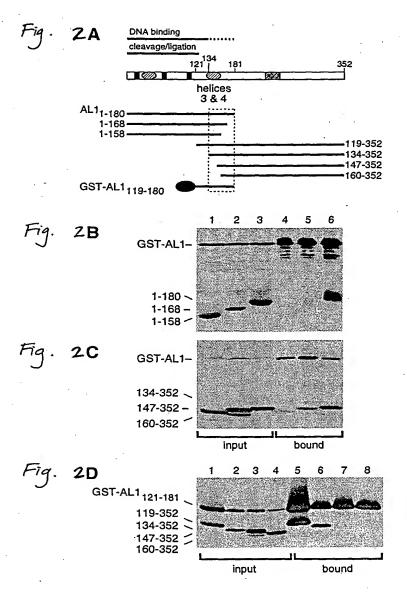
TLVWGE<u>AA</u>VD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:9)

Ala14 mutant:

TLVWGEFQV<u>A</u> GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:10)

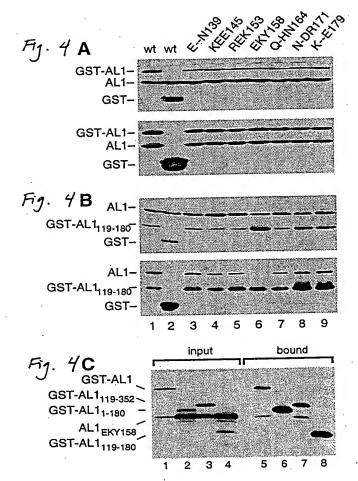
Leu mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDLLLEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:11)



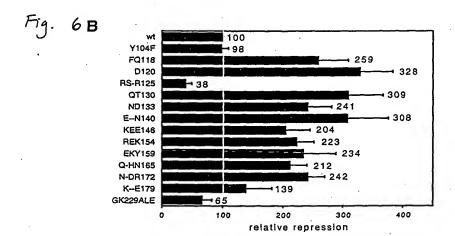
FQ118 D120 RS-R125 QT130 ND133 E--N140 KEE146 REK154 EKY159 Q-HN165 N-DR172 K--E179 COTSNDAAAEALNASSKEEALQIIREKIPEKYLFQFHNLNSNLDRIFDKTPEP helix 3 helix 4 A ‡ · + + ‡ ‡ ‡ ‡ ‡ £ 1

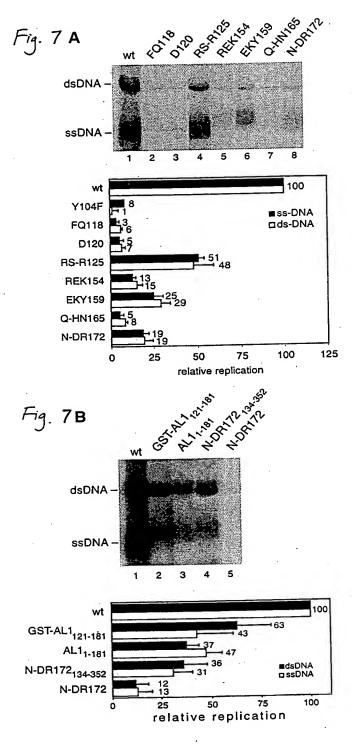
core oligomerization domain

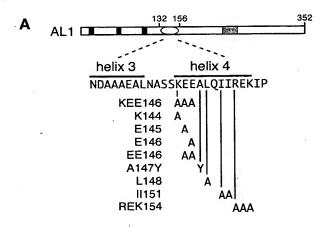


REK154 EKY-159 0 Q-HN165 wild type FQ118 D120 RS-R125 R122 S123 R125 QT130 ND133 AAA136 E-N140 KEE146 6 60 80 AL1/AL1 (rel. int.) 8 I õ 95 120 140 REKY-159
G-HN165
N-DR172
K--E179 wild type FO118 D120 RS-R125 O.5 R122 S123 R125 OT130 ND133 AAA136 E-N140 KEE 146 8 60 80 100 AL 1/mRb (rel. int.) T I 107 120 140 1 135

160







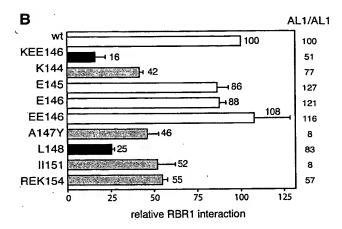


Fig. 9

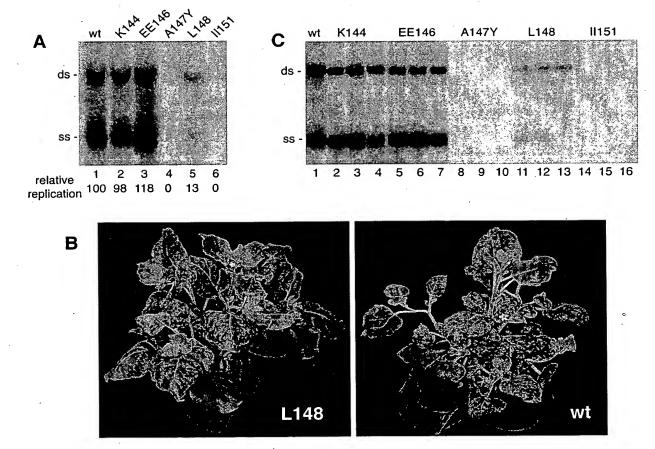
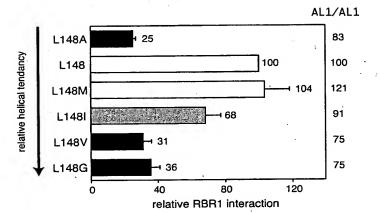
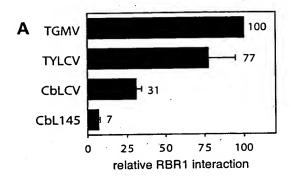


Fig.10





TGMV KEEALQIIREKIP

TYLCV-DR KSEALKILRELAP

CbLCV VEEALAIIRAGDP

consensus (±)₁₋₃AL×IIRE××P
D